

GenCore Version 5.1.6
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OM protein - protein search, using swi model

Run on: June 25, 2003, 14:40:41 ; Search time 12.6202 Seconds

(Without alignments)
837.928 Million cell updates/sec

Title: US-09-622-613b-24

Perfect score: 601

Sequence: 1 SNAATFOQHIIITPIICNT.....ICVKEQYVHFAGIGRCP 110

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	586.5	97.6	111	2 A27121	ribonuclease-relat
2	450	74.9	111	1 JX0120	pancreatic ribonuc
3	369	51.4	111	2 JX0085	pancreatic ribonuc
4	272.5	45.3	104	2 A39035	ribonuclease-relat
5	135.5	22.5	124	1 NRWHR	pancreatic ribonuc
6	135.5	22.5	145	1 A35932	angiogenin precurs
7	133.5	22.2	167	2 S20066	pancreatic-type ri
8	132.5	22.0	124	1 NRPQ	pancreatic ribonuc
9	126.5	21.0	119	2 S41111	pancreatic ribonuc
10	122.5	20.4	124	1 NRPRH	pancreatic ribonuc
11	122	20.3	122	1 NRKGR	pancreatic ribonuc
12	120.5	20.0	128	1 NRCU	pancreatic ribonuc
13	120.5	20.0	149	1 NRMS	pancreatic ribonuc
14	119.5	19.9	123	1 A43825	angiogenin - pig
15	118.5	19.7	128	1 NRGPB	pancreatic ribonuc
16	117.5	19.6	128	1 NRHO	pancreatic ribonuc
17	116.5	19.4	124	1 NRCH	pancreatic ribonuc
18	116.5	19.4	124	1 NRCHM	pancreatic ribonuc
19	116.5	19.4	124	1 NRCHM	pancreatic ribonuc
20	116.5	19.4	124	1 NRCHM	pancreatic ribonuc
21	114.5	19.1	124	2 S08549	pancreatic ribonuc
22	114	19.0	125	1 A32474	ribonuclease - dom
23	113.5	18.9	124	1 NRDN	angiogenin (valida
24	113.5	18.9	125	1 B43825	pancreatic ribonuc
25	113	18.8	147	1 NRHUG	angiogenin - rabbi
26	112.5	18.7	124	1 NRGE	angiogenin precurs
27	112.5	18.7	124	1 NRDEO	pancreatic ribonuc
28	111.5	18.6	130	2 S22808	pancreatic ribonuc
29	110.5	18.4	124	1 NRBOB	pancreatic ribonuc

30	110.5	18.4	124	1 NRWB	pancreatic ribonuc
31	110.5	18.4	124	1 NREKN	pancreatic ribonuc
32	110.5	18.4	124	2 S07141	pancreatic ribonuc
33	110.5	18.4	124	2 JCS560	pancreatic ribonuc
34	110.5	18.4	150	2 NRBO	pancreatic ribonuc
35	110.5	18.4	158	2 I61900	pancreatic ribonuc
36	109.5	18.2	124	1 NRSH	pancreatic ribonuc
37	108.5	18.1	119	2 JX0115	pancreatic ribonuc
38	108.5	18.1	124	1 NRCH	pancreatic ribonuc
39	108.5	18.1	152	1 NRCH	pancreatic ribonuc
40	106.5	17.7	124	1 NRHP	pancreatic ribonuc
41	106.5	17.7	125	4 A47498	pancreatic ribonuc
42	106.5	17.7	150	1 NRBO	pancreatic ribonuc
43	104.5	17.4	124	1 NRGN	pancreatic ribonuc
44	104.5	17.4	124	1 NRDE	pancreatic ribonuc
45	104	17.3	125	2 S04503	pancreatic ribonuc

ALIGNMENTS

RESULT 1

A27121 ribonuclease-related stallo acid-binding lectin - bullfrog

C:Species: Rana catesbeiana (bullfrog)

C:Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 30-Jun-1993

C:Accession: A27121

R:Titani, K., Takio, K., Kuwada, M., Nitta, K., Sakakibara, F., Kawachi, H., Takayan

Biochemistry 26, 2189-2194, 1987

A:Title: Amino acid sequence of stallo acid-binding lectin from frog (Rana catesbeiana

A:Reference number: A27121; MUID:87299649; PMID:3304421

A:Accession: A27121

A:Molecule type: protein

A:Residues: 1-111 <TTT>

C:Superfamily: pancreatic ribonuclease

C:Keywords: lectin

Query Match

Best Local Similarity

Matches 109; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Query Match

Best Local Similarity

Matches 86; Conservative 7; Mismatches 15; Indels 2;

Query Match

Best Local Similarity

Matches 86; Conservative 7; Mismatches 15; Indels 2;

Query Match

Best Local Similarity

Matches 86; Conservative 7; Mismatches 15; Indels 2;

Query Match

Best Local Similarity

Matches 86; Conservative 7; Mismatches 15; Indels 2;

QY 2 NMATFOCKHIITNP-IICNTIMDNNIYVGGCKRVNFTFISSATVKAICTGY-IMNV 59
 DB 2 NMAFKCKHPISTINCNITMDKSIYVGGCKERNFTFISSATVKAICSGASTNRV 61
 QY 60 LSTRFOLNCTRTSITPRPCPYSSRTETNYICVCKENQYVHFAGIGRC 109
 DB 62 LSTRFOLNCTRTSATAPRCPYNSRTETNYICVCKENRLPVHFAGIGRC 111

RESULT 3

JX0085
 pancreatic ribonuclease (EC 3.1.27.5) - bullfrog
 C:Species: Rana catesbeiana (bullfrog)
 C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 05-Aug-1994
 C:Accession: JX0085
 R:Nilta, R.; Katayama, N.; Okabe, Y.; Iwama, M.; Matanabe, H.; Abe, Y.; Okazaki, T.; Ohg
 J. Biochem. 106, 729-735, 1989
 A:Title: Primary structure of a ribonuclease from bullfrog (Rana catesbeiana) liver.
 A:Reference number: JX0085; MUID:90130374; PMID:2613682
 A:Accession: JX0085
 A:Molecule type: protein
 A:Residues: 1-111 <NIT>
 C:Superfamily: pancreatic ribonuclease
 C:Keywords: hydrolase; pyroglytamic acid
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F:10/35/104/Active site: His, Lys, His #status predicted
 F:19-72/34-82/52-97/94-111/Disulfide bonds: #status predicted

Query Match 61.4%; Score 369; DB 2; Length 111;
 Best Local Similarity 65.5%; Pred. No. 9.8e-30;
 Matches 72; Conservative 9; Mismatches 27; Indels 2; Gaps 2;

QY 2 NMATFOCKHIITNP-II-CNTIMDNNIYVGGCKRVNFTFISSATVKAICTGYT-IMNV 59
 DB 2 NMAFKCKHPISTISIDCNITMDKAIYVGGCKERNFTFISSDNKKAICSGVSPBKE 61
 QY 60 LSTRFOLNCTRTSITPRPCPYSSRTETNYICVCKENQYVHFAGIGRC 109
 DB 62 LSTRFOLNCTRTSITPRPCPYHSPDNKKAICVCKEQLPVHFAGIGRC 111

RESULT 4

A39035
 ribonuclease-related anti-tumor protein - northern leopard frog (fragment)
 C:Species: Rana pipiens (northern leopard frog)
 C>Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 30-Jun-1993
 C:Accession: A39035
 R:Ardelet, W.; Mikulski, S.M.; Shogen, K.
 J. Biol. Chem. 266, 245-251, 1991
 A:Title: Amino acid sequence of an anti-tumor protein from Rana pipiens oocytes and earl
 A:Reference number: A39035; MUID:91093131; PMID:1985896
 A:Accession: A39035
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-104 <ARD>
 C:Superfamily: pancreatic ribonuclease

Query Match 45.3%; Score 272.5; DB 2; Length 104;
 Best Local Similarity 49.1%; Pred. No. 3.5e-20;
 Matches 54; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

QY 2 NMATFOCKHIITNP-IIICNTIMDNNIYVGGCKRVNFTFISSATVKAICTGYT-IMNV 59
 DB 2 DMLFQCKHITNTRDVCNDIMSTNLF----HCKDKMTFIYSRPEPKAICKGIIASKNV 57
 QY 60 LSTRFOLNCTRTSITPRPCPYSSRTETNYICVCKENQYVHFAGIGRC 109
 DB 58 LTTSEFLSDC---NVTSRCKYKLRKSTNKFVTCENQAPVHFVGVSC 104

RESULT 5

NRMHK
 pancreatic ribonuclease (EC 3.1.27.5) - minke whale

N:Alternate names: RNase A
 C:Species: Balaenoptera acutorostrata (minke whale, lesser rorqual)
 C>Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 03-Jun-1994
 C:Accession: A00818
 R:Emmens, M.; Wellings, G.W.; Beintema, J.J.
 Biochem. J. 157, 317-323, 1976
 A:Title: The amino acid sequence of pike whale (lesser rorqual) pancreatic ribonuclea
 A:Reference number: A00818; MUID:76277855; PMID:962870
 A:Accession: A00818
 A:Molecule type: protein
 A:Residues: 1-124 <EMM>
 C:Superfamily: pancreatic ribonuclease
 C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
 F:12/41/119/Active site: His, Lys, His #status predicted
 F:26-84/40-95/58-110/65-72/Disulfide bonds: #status predicted
 F:76/Binding site: carbohydrate (asn) (covalent) (partial) #status experimental

Query Match 22.5%; Score 135.5; DB 1; Length 124;
 Best Local Similarity 33.3%; Pred. No. 1.7e-06;
 Matches 39; Conservative 16; Mismatches 39; Indels 23; Gaps 7;

QY 6 FQCKHIIT-----NTPICNTIMDNNIYVGGCKRVNFTFISSATVKAICTGYIMNV 59
 DB 8 FQCKHIITNTPICNTIMDNNIYVGGCKRVNFTFISSATVKAICTGYIMNV 59
 QY 60 L-----STRFOLNCTRTSITPR-CPYSSRTETNYICVCKE-NQY-PVHF 103
 DB 64 LCKKGRNCTYENSTMTHTDCKRQYKSKYPRCAKTKQKKEHIVACEGNPVYVHF 120

RESULT 6

A35932
 angiogenin precursor - mouse
 N:Alternate names: angiogenesis factor
 N:Contains: ribonuclease (EC 3.1.27.-)
 C:Species: Mus musculus (house mouse)
 C>Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 18-Jun-1999
 C:Accession: A35932
 R:Bond, M.D.; Vallee, B.L.
 Biochem. Biophys. Res. Commun. 171, 988-995, 1990
 A:Title: Isolation and sequencing of mouse angiogenin DNA.
 A:Reference number: A35932; MUID:91025023; PMID:2224258
 A:Accession: A35932
 A:Status: not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-145 <BDN>
 A:Cross-references: GB:U22516; NID:g726325; PIDN:AAA91366.1; PID:g726326
 C:Genetics:
 A:Introns: #status absent
 C:Function:
 A:Description: hydrolyzes rRNA; induces vascularization of normal and malignant tissu
 C:Superfamily: pancreatic ribonuclease
 C:Keywords: angiogenesis; hydrolase; nucleic acid degradation; pyroglytamic acid
 F:1-24/Domain: signal sequence #status predicted <SIG>
 F:25-145/Product: angiogenin #status predicted <MAT>
 F:25/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predic
 F:37/64/137/Active site: His, Lys, His #status predicted
 F:50-104/63-115/81-130/Disulfide bonds: #status predicted

Query Match 22.5%; Score 135.5; DB 1; Length 145;
 Best Local Similarity 39.5%; Pred. No. 2e-06;
 Matches 30; Conservative 12; Mismatches 29; Indels 5; Gaps 3;

QY 33 CKRVNFTFISSATVKAIC---GVIMNV-LSTRFOLNCTRTSITPR-CPYSSRTE 87
 DB 63 CKRVNFTFIHGKSKIKATCGANSPYRENLRMSKSPQVTTCKHTGGSPRPPCYRASAG 122
 QY 88 TNYICVCKENQYVHF 103
 DB 123 FRHVIVACENGDLPVHF 138

RESULT 7

Db 6 AKFERQHDIDNPSVSSNYCNQMKSR-NLTGCRKCPVNTFVHESLADVOAVCS---QK 61
QY 58 NVL-----STTRFQNTCTRTSTTRP-CPYSSRTETNYICVCE-NQY-PVHF 103
Db 62 NVAKNGQTCNYQSVSTMSITDCRETSGSKIPNCAKYTKQAKKHIIIVACEGPNYPVHF 120

RESULT 11

NRKCR
pancreatic ribonuclease (EC 3.1.27.5) - red kangaroo
N:Alternate names: RNase 1; RNase A
C:Species: Macropus rufus, Megaleia rufa (red kangaroo)
C:Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 04-Oct-1996
C:Accession: A00833
R:Gastra, W.; Welling, G.W.; Beintema, J.J.
A:Title: The amino-acid sequence of kangaroo pancreatic ribonuclease.
A:Reference number: A00833; MUID:78190621; PMID:658039
A:Accession: A00833
A:Molecule type: protein
A:Residues: 1-122 <GMA>
C:Superfamily: pancreatic ribonuclease
C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F:11,40,117/Active site: His, Lys, His #status predicted
F:25-83,39-94,57-109,64-71/Disulfide bonds: #status predicted
F:61/Binding site: carbohydrate (Asn) (covalent) #status absent

Query Match

20.3%; Score 122; DB 1; Length 122;
Best Local Similarity 30.7%; Pred. No. 3.7e-05;
Matches 35; Conservative 16; Mismatches 45; Indels 18; Gaps 6;

QY 6 FQOKHI-----INTPIICNTIMDNNIYVGGCKRVMTFISSATYKAICTGVINNV 51
Db 7 FQOKHMDTSTRASSNYCNLMKAR-DMTSGRCPLNFIHPKSVDAVCEQENVTCK 65
QY 52 TGVINNVLTSTFQNTCTRTSTTRP-CPYSSRTETNYICVCE-NQY-PVHF 103
Db 66 NGRTNC-YKSNRSLSTTRKOTGASKYPCQYETSMNLKQIIIVACEGQYVPHF 118

RESULT 12

NRUCU

pancreatic ribonuclease (EC 3.1.27.5) - nutria (tentative sequence)
N:Alternate names: RNase 1; RNase A
C:Species: Myocastor coypus (nutria, coypu)
C:Date: 24-Apr-1984 #sequence_revision 30-Sep-1988 #text_change 31-Mar-2000
C:Accession: A00822
R:van den Berg, A.; van den Hende-Timmer, L.; Beintema, J.J.
Biochim. Biophys. Acta 453, 400-409, 1976
A:Title: Isolation, properties and primary structure of coypu and chinchilla pancreatic
A:Reference number: A90612; MUID:77065676; PMID:99896
A:Accession: A00822
A:Molecule type: protein
A:Residues: 1-128 <VAN>
C:Superfamily: pancreatic ribonuclease
C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F:12,41,119/Active site: His, Lys, His #status predicted
F:26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
F:34/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 20.0%; Score 120.5; DB 1; Length 128;
Best Local Similarity 31.6%; Pred. No. 5.5e-05;
Matches 37; Conservative 15; Mismatches 42; Indels 23; Gaps 7;

QY 6 FQOKHI-----INTPIICNTIMDNNIYVGGCKRVMTFISSATYKAICTGVINNV 59
Db 8 FERQHMDSRSPSTNPVNCNEMKSR-NMTOGRKCPVNTFVHEPLADVOAVC---FQKNV 63
QY 60 L-----STTRFQNTCTRTSTTRP-CPYSSRTETNYICVCE-NQY-PVHF 103
Db 64 LCKNGQTCNYQSVSTMSITDCRETSGSKIPNCAKYTKQAKKHIIIVACEGPNYPVHF 120

RESULT 13

NRMS

pancreatic ribonuclease (EC 3.1.27.5) precursor - mouse
N:Alternate names: RNase 1; RNase A
C:Species: Mus musculus (house mouse)
C:Date: 30-Nov-1980 #sequence_revision 13-Mar-1997 #text_change 18-Jun-1999
C:Accession: A34090; MUID:92107684; PMID:1840677
R:Schueller, C.; Nijssen, H.M.J.; Kok, R.; Beintema, J.J.
Mol. Biol. Evol. 7, 29-44, 1990
A:Title: Evolution of nucleic acids coding for ribonucleases: the mRNA sequence of mo
A:Reference number: A34090; MUID:90136034; PMID:2299980
A:Accession: A34090
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-149 <SCH>
A:Cross-references: GB:M27814; NID:9200762; PIDN:AAA0060.1; PID:9200763
R:Samuelson, L.C.; Wiehner, K.; Howard, G.; Schmidt, R.M.; Koepflin, D.; Meisler, M.H.
Nucleic Acids Res. 19, 6935-6941, 1991
A:Title: Isolation of the murine ribonuclease gene R1b-1: structure and tissue specif
A:Reference number: S22598; MUID:92107684; PMID:1840677
A:Accession: S22598
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-149 <SAM>
A:Cross-references: EMBL:X60103; NID:953981; PIDN:CAA42697.1; PID:953982
R:Lenstra, J.A.; Beintema, J.J.
Eur. J. Biochem. 98, 399-408, 1979
A:Title: The amino acid sequence of mouse pancreatic ribonuclease.
A:Reference number: A00830; MUID:80024269; PMID:556267
A:Accession: A00830
A:Molecule type: protein
A:Residues: 26-149 <LEN>
C:Superfamily: pancreatic ribonuclease
C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F:1-25/Domain: signal sequence #status predicted <Sig>
F:26-149/Product: pancreatic ribonuclease #status experimental <Mat>
F:37,66,144/Active site: His, Lys, His #status predicted
F:51-109,65-120,83-135,90-97/Disulfide bonds: #status predicted
F:52,87/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match

20.0%; Score 120.5; DB 1; Length 149;
Best Local Similarity 30.8%; Pred. No. 6.4e-05;
Matches 36; Conservative 16; Mismatches 42; Indels 23; Gaps 7;

QY 6 FQOKHI-----INTPIICNTIMDNNIYVGGCKRVMTFISSATYKAICTGVINNV 59
Db 33 FQOKHMDPDGSSINSPTFCNQMKRR-DMTNSCKPVTMFVHEPLADVOAVCS---QENV 88
QY 60 L-----STTRFQNTCTRTSTTRP-CPYSSRTETNYICVCE-NQY-PVHF 103
Db 89 TCKNRKSNQYSSSLHTTDCGLKGNKRYPCNDYKTYOKHIIIVACEGPNYPVHF 145

RESULT 14

A43825

angiotensin - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S29834; A43825
R:Bond, M.D.; Strydom, P.J.; Vallee, B.L.
Biochim. Biophys. Acta 1162, 177-186, 1993
A:Title: Characterization and sequencing of rabbit, pig and mouse angiotensins: discer
A:Reference number: S29833; MUID:93192291; PMID:8448182
A:Accession: S29834
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-123 <BON>
A>Note: this sequence was submitted to the Protein Sequence Database, December 1992

C:Superfamily: pancreatic ribonuclease

Query Match 19.9%; Score 119.5; DB 1; Length 123;
Best Local Similarity 39.5%; Pred. No. 6.6e-05;
Matches 30; Conservative 6; Mismatches 35; Indels 5; Gaps 2;

